FIG. 1-1

Human Basic Fibroblast Growth Factor

```
        10         20         30         40         50         60         70
AATTCATGCC TCTTTCTCTC CTTTTGTTGG TAGACGACTT CAGCCTCTGT CCTTTAATTT TAAAGTTTAT

        80         90        100        110        120        130        140
GCCCCACTTG TACCCCTCGT CTTTTGGTGA TTTAGAGATT TTCAAAGCCT GCTCTGACAC AGACTCTTCC

       150        160        170        180        190        200        210
TTGGATTGCA ACTTCTCTAC TTTGGGGTGG AAACGGCTTC TCCGTTTTGA AACGCTAGCG GGGAAAAAAT

       220        230        240        250        260        270        280
GGGGGAGAAA GTTGAGTTTA AACTTTTAAA AGTTGAGTCA CGGCTGGTTG CGCACGAAAA GCCCCGCAGT

       290        300        310        320        330        340        350
GTGGAGAAAG CCTAAACGTG GTTTGGGTGG TGCGGGGGTT GGGCGGGGGT GACTTTTGGG GGATAAGGGG

       360        370        380        390        400        410        420
CGGTGGAGCC CAGGGAATGC CAAAGCCCTG CCGCGGCCTC CGACGCGCGC CCCCCGCCCC TCGCCTCTCC

       430        440        450        460        470        480        490
CCCGCCCCCG ACTGAGGCCG GGCTCCCCGC CGGACTGATG TCGCGCGCTT GCGTGTTGTG GCCGAAGCCG

       500        510        520        530        540        550        560
CCGAACTCAG AGGCCGGCCC CAGAAAACCC GAGCGAGTAG GGGGCGGCGC GCAGGAGGGA GGAGAACTGG

       570        580        590        600        610        620        630
GGGCGCGGGA GGCTGGTGGG TGTGGGGGGT GGAGATGTAG AAGATGTGAC GCCGCGGCCC GGCGGGTGCC

       640        650        660        670        680        690        700
AGATTAGCGG ACGGCTGCCC GCGGTTGCAA CGGGATCCCG GGCGCTGCAG CTTGGGAGGC GGCTCTCCCC

       710        720        730        740        750        760        770
AGGCGGCGTC CGCGGAGACA CCCATCTGTG AACCCCAGGT CCCGGGCCGC CGGCTCGCCG CGCACCAGGG

       780        790        800        810        820        830        840
GCCGGCGGAC AGAAGAGCGG CCGAGCGGCT CGAGGCTGGG GGACCGCGGG CGCGGCCGCG CGCTGCCGGG

       850        860        870        880        890        900        910
CGGGAGGCTG GGGGGCCGGG GCCGGGGCCG TGCCCGGAGC GGGTCGGAGG CCGGGGCCGG GGCCGGGGGA

       920        930        940        950        960
CGGCGGCTCC CCGCGCGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC GCAGGGACC ATG GCA GCC
                                                                 Met Ala Ala

    984                     999                     1014                    1029
GGG AGC ATC ACC ACG CTG CCC GCC TTG CCC GAG GAT GGC GGC AGC GGC GCC TTC CCG
Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro

        1044                    1059                    1074                    1089
CCC GGC CAC TTC AAG GAC CCC AAG CGG CTG TAC TGC AAA AAC GGG GGC TTC TTC CTG
Pro Gly His Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
```

FIG. 1-2

```
          1104                1119                1134                1149
CGC ATC CAC CCC GAC GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC
Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile

               1164                1179                1194
AAG CTA CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT GCT
Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala

                    1224                1239                1254
AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT AAA TGT GTT ACG
Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr

   1269                1284                1299                1314
GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT AAC TAC AAT ACT TAC CGG TCA
Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser

       1329                1344                1359                1374
AGG AAA TAC ACC AGT TGG TAT GTG GCA TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA
Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly

          1389                1404                1419                1434
TCC AAA ACA GGA CCT GGG CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC
Ser Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser

              1450        1460        1470        1480        1490        1500
TGA TTT TAATGGCCAC ATCTAATCTC ATTTCACATG AAAGAAGAAG TATATTTTAG AAATTTGTTA


      1510        1520        1530        1540        1550        1560        1570
ATGAGAGTAA AAGAAAATAA ATGTGTATAG CTCAGTTTGG ATAATTGGTC AAACAATTTT TTATCCAGTA

      1580        1590        1600        1610        1620        1630        1640
GTAAAATATG TAACCATGCC CAGTAAAGAA AAATAACAAA AGTTGTAAAA TGTATATTCT CCCTTTTATA

      1650        1660        1670        1680        1690        1700        1710
TTGCATCTGC TGTTACCCAG TGAAGCTTAC CTAGAGCAAT GATCTTTTTC ACGCATTTGC TTTATTCGAA

      1720        1730        1740        1750        1760        1770        1780
AAGAGGCTTT TAAAATGTGC ATGTTTAGAA AACAAAATTT CTTCATGGAA ATCATATACA TTAGAAAATC

      1790        1800        1810        1820        1830        1840        1850
ACAGTCAGAT GTTTAATCAA TCCAAAAATG TCCACTATTT CTTATGTCAT TCGTTAGTCT ACATGTTTCT

      1860        1870        1880        1890        1900        1910        1920
AAACATATAA ATGTGAATTT AATCAATTCC TTTCATAGTT TTATAATTCT CTGGCAGTTC CTTATGATAG

      1930        1940        1950        1960        1969
AGTTTATAAA ACAGTCCTGT GTAAACTGCT GGAAGTTCTT CCGGAATTC
```

FIG. 2

Human Acidic FGF

```
                                        27                                  54
TGC ATT TTG TGC CTT TGC TGG AAG AAC CGA CTA CAG GTT TGT TCA ATT TCT TAC

                                        81                                 108
AGT CTT GAA AGC GCC ACA AGC AGC AGC TGC TGA GCC ATG GCT GAA GGG GAA ATC
                                                 MET Ala Glu Gly Glu Ile
                                                  1

                                       135                                 162
ACC ACC TTC ACA GCC CTG ACC GAG AAG TTT AAT CTG CCT CCA GGG AAT TAC AAG
Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys
          10                                                20

                                       189                                 216
AAG CCC AAA CTC CTC TAC TGT AGC AAC GGG GGC CAC TTC CTG AGG ATC CTT CCG
Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro
                    30                                            40

                                       243                                 270
GAT GGC ACA GTG GAT GGG ACA AGG GAC AGG AGC GAC CAG CAC ATT CAG CTG CAG
Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
                                50                                        60

                                       297                                 324
CTC AGT GCG GAA AGC GTG GGG GAG GTG TAT ATA AAG AGT ACC GAG ACT GGC CAG
Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
                                    70

                                       351                                 378
TAC TTG GCC ATG GAC ACC GAC GGG CTT TTA TAC GGC TCA CAG ACA CCA AAT GAG
Tyr Leu Ala MET Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
      80                                            90

                                       405                                 432
GAA TGT TTG TTC CTG GAA AGG CTG GAG GAG AAC CAT TAC AAC ACC TAT ATA TCC
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser
          100                                               110

                                       459                                 486
AAG AAG CAT GCA GAG AAG AAT TGG TTT GTT GGC CTC AAG AAG AAT GGG AGC TGC
Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys
                    120                                           130

                                       513                                 540
AAA CGC GGT CCT CGG ACT CAC TAT GGC CAG AAA GCA ATC TTG TTT CTC CCC CTG
Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu
                                140                                   150

                                       567                                 594
CCA GTC TCT TCT GAT TAA AGA GAT CTG TTC TGG GTG TTG ACC ACT CCA GAG AAG
Pro Val Ser Ser Asp
                155

                                       621
TTT CGA GGG GTC CTC ACC TGG TTG ACC CAA AAA TGT TCC CTT GA
```

Comparison of amino acid sequence of
human basic and acidic FGF

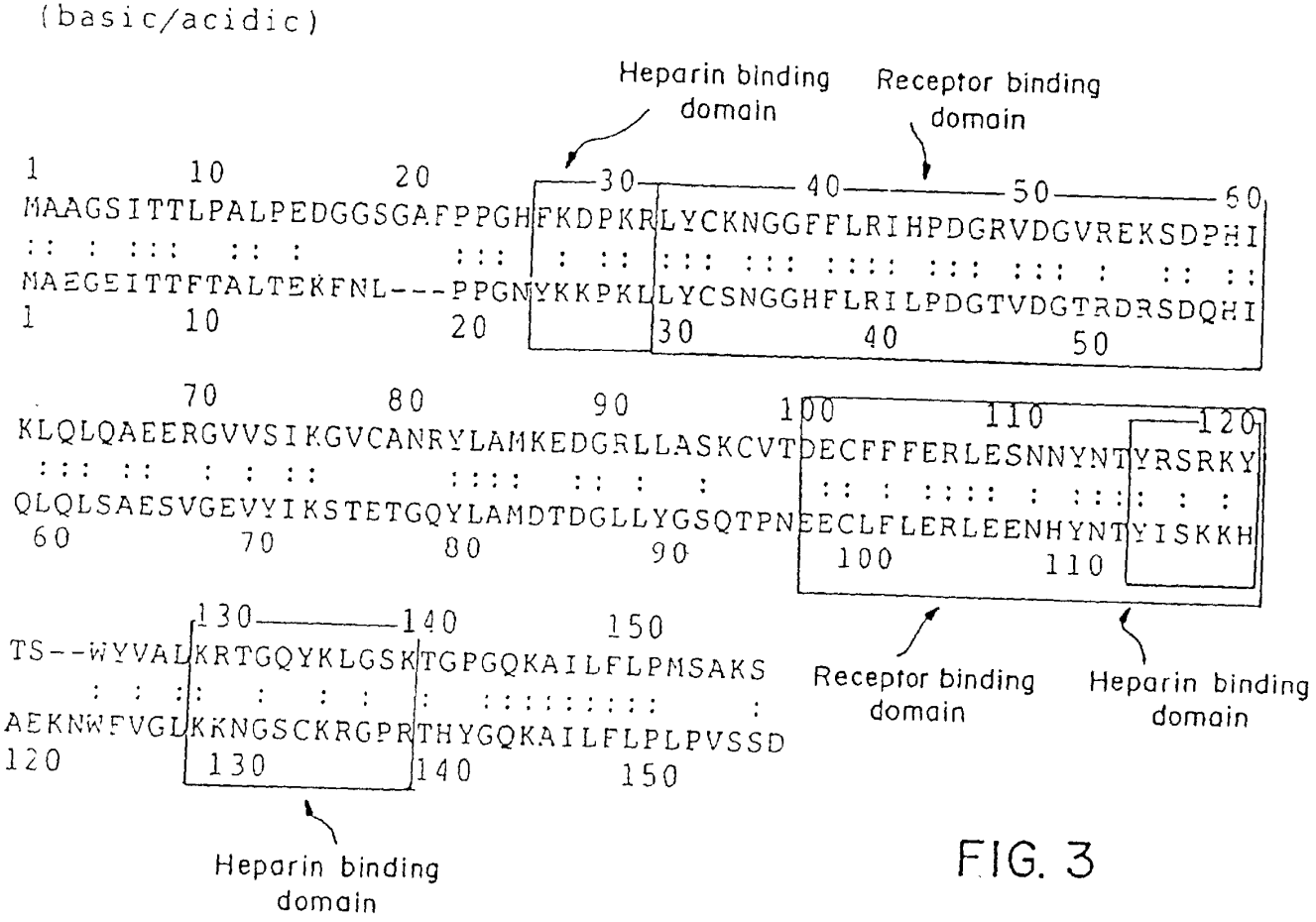

FIG. 3

APPLN. FILING DATE: JULY 9, 2001
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APPLICATION SERIAL NO: 09/902,460

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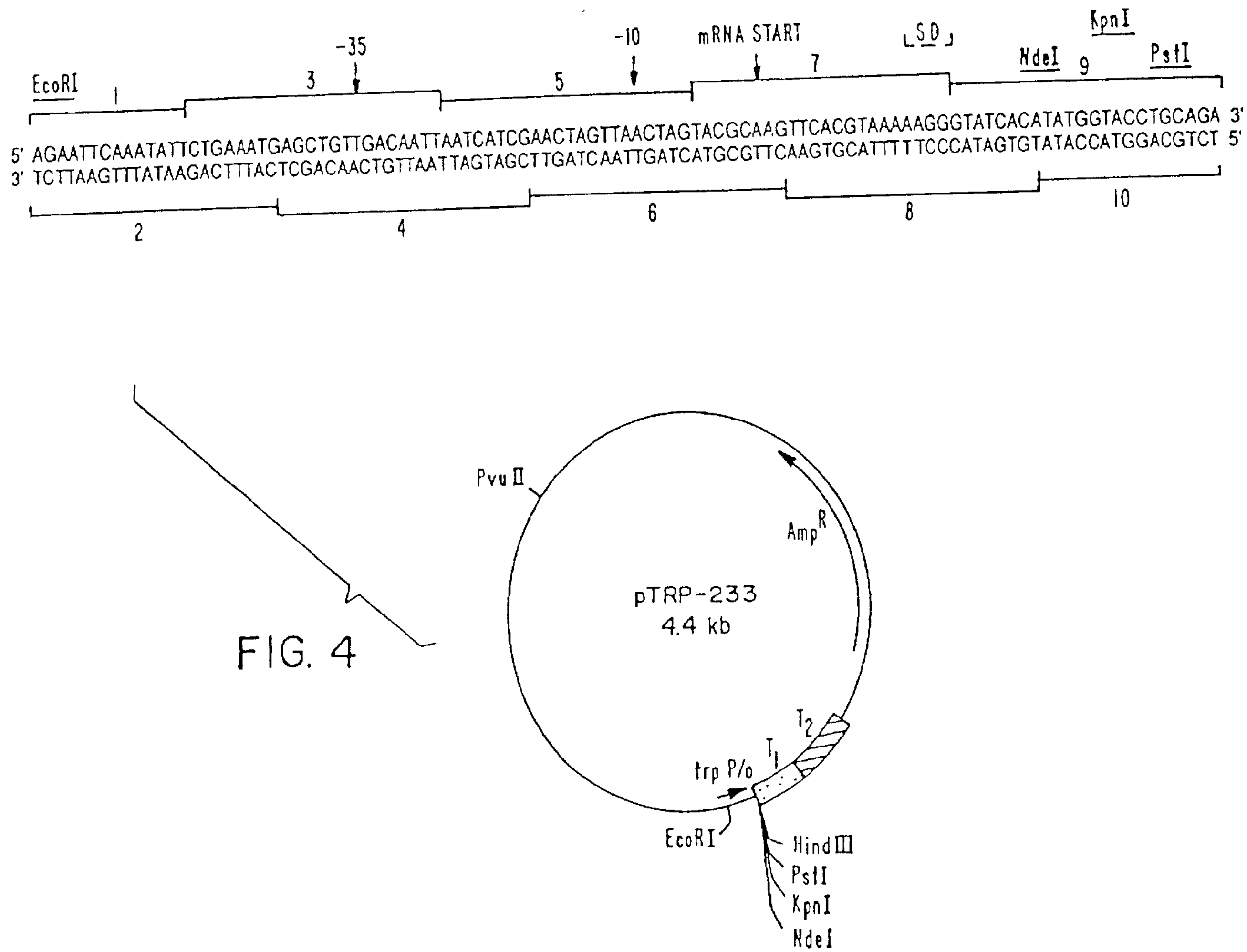
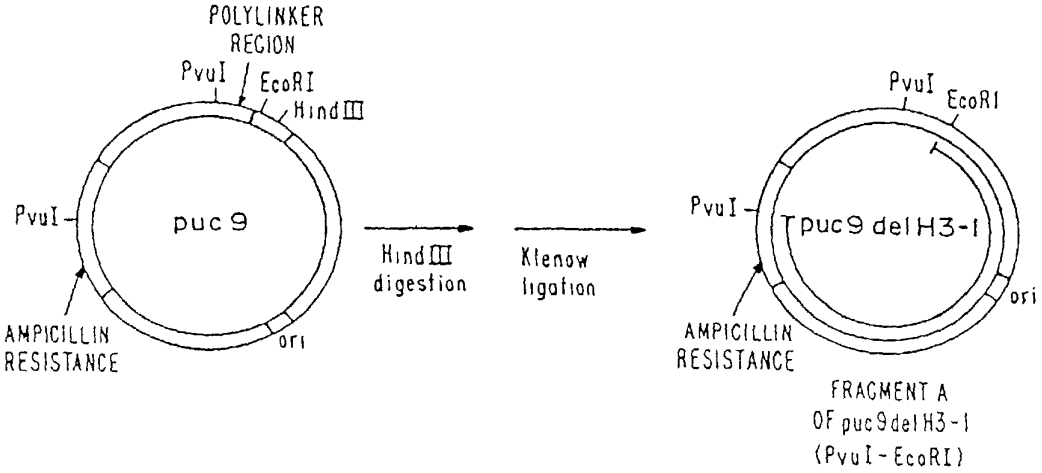


FIG. 4


POLYLINKER
REGION
PvuI
EcoRI
HindIII
puc 9
PvuI
AMPICILLIN
RESISTANCE
ori
HindIII
digestion
Klenow
ligation
PvuI
EcoRI
PvuI
puc9 delH3-1
ori
AMPICILLIN
RESISTANCE
FRAGMENT A
OF puc9delH3-1
(PvuI-EcoRI)

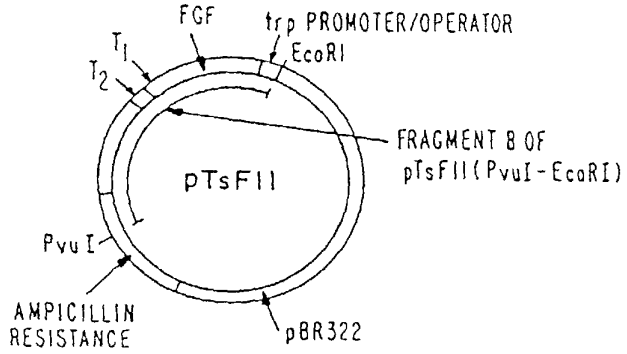
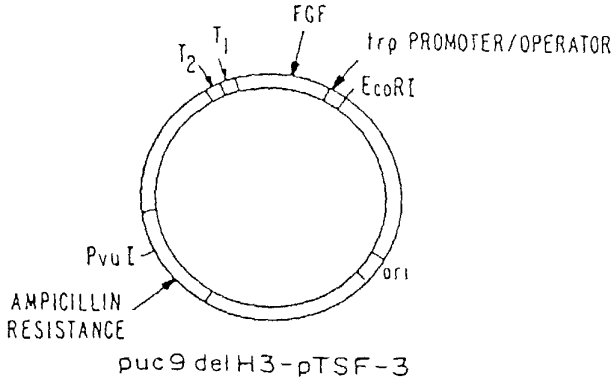

FGF
trp PROMOTER/OPERATOR
T1
T2
EcoRI
FRAGMENT B OF
pTsF11(PvuI-EcoRI)
pTsF11
PvuI
AMPICILLIN
RESISTANCE
pBR322

FIG. 5


FGF
T1
T2
trp PROMOTER/OPERATOR
EcoRI
PvuI
ori
AMPICILLIN
RESISTANCE
puc9 delH3-pTSF-3

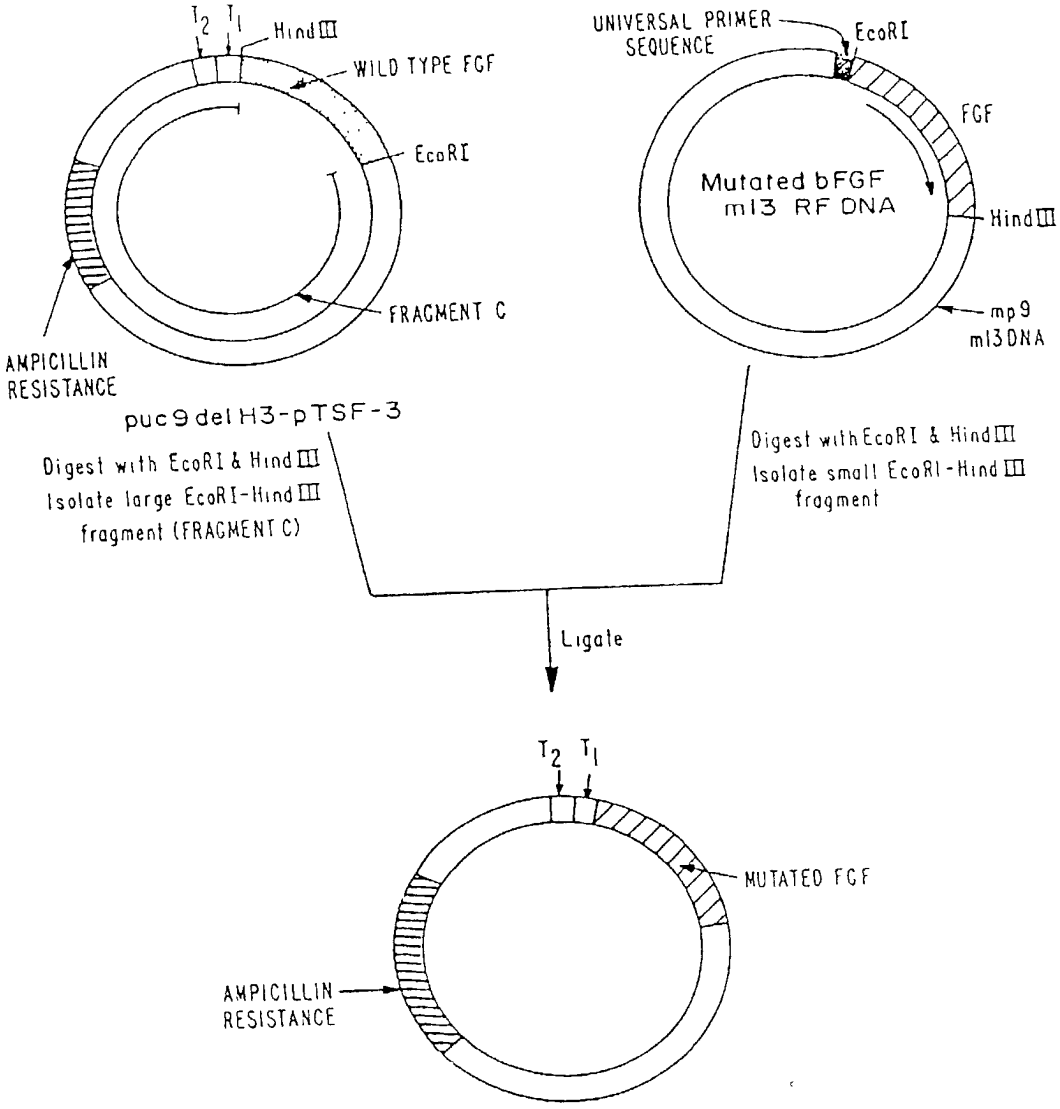

T2 T1
HindIII
WILD TYPE FGF
EcoRI
FRAGMENT C
AMPICILLIN RESISTANCE
puc9 del H3-pTSF-3
Digest with EcoRI & HindIII
Isolate large EcoRI-HindIII fragment (FRAGMENT C)
UNIVERSAL PRIMER SEQUENCE
EcoRI
FGF
Mutated bFGF m13 RF DNA
HindIII
mp9 m13DNA
Digest with EcoRI & HindIII
Isolate small EcoRI-HindIII fragment
Ligate
T2 T1
MUTATED FGF
AMPICILLIN RESISTANCE

FIG. 6

FIG. 7